

Figure 4A: Aligned hedg-5 cDNA and predicted amino acid sequence. The first 250 bp of DNA sequence (lower case) is derived from genomic DNA flanking the 5' end of the cDNA insert from clone pC3-hedg5-3. Sequences from nt 251-1523 are shown in lower case wherever apparent polymorphisms in different human clones were found. Coding region polymorphisms are detailed in Table 1. One intron exists within the coding region of hedg-5, located between nt 996/997 of the cDNA sequence shown.

1 cacccttcctaacctgagcgccctagcctgggaaacaaacaattaaaatgtgcgctaaatg 60
-----+-----+-----+-----+-----+-----+-----+
gtggaaggattggactcgccgatcggaacctttgtttgttaattttacacgcgatttac
61 ctgtggtaggaggtcaggggctatgtcctggaccaaaggacatttgcactgagacctgac 120
-----+-----+-----+-----+-----+-----+-----+
gacaccatcctccagtcctccgatacaggacctggtttcctgtaaacgtgactctggactg
121 acttcaggtcttcaactcccttgatgggagttagccagaacgggcttagaaacagcaatt 180
-----+-----+-----+-----+-----+-----+-----+
tgaagtccagaagttgaggggaactaccctcaatcggtcttgcccgaatctttgtcgttaa
181 gatggcttagtgactgattttacaaatgatatttgtttcttctttaattctttcttagg 240
-----+-----+-----+-----+-----+-----+-----+
ctaccgaatcactgactaaaatgtttactataaacaagaagaatttaaaagaagatcc
M N E C H Y D K H M D F F Y
241 atgttcacttCTTCTCCACAATGAATGAGTGTCACTATGACAAGCACATGGACTTTTTTT 300
-----+-----+-----+-----+-----+-----+-----+
tacaagtgaagaagAGGTGTTACTTACTCACAGTGATACTGTTCTGTACCTGAAAAAAA
N R S N T D T V D D W T G T K L V I V L
301 ATAATAGGAGCAACACTGATACTGTGATGACTGGACAGGAACAAAGCTTGTGATTGTTT 360
-----+-----+-----+-----+-----+-----+-----+
TATTATCCTCGTTGTGACTATGACAGCTACTGACCTGTCCTTGTTTCGAACACTAACAA
C V G T F F C L F I F F S N S L V I A A
361 TGTGTGTTGGGACGTTTTTCTGCCTGTTTATTTTTTTTTTCTAATTCTCTGGTCATCGCGG 420
-----+-----+-----+-----+-----+-----+-----+
ACACACAACCCTGCAAAAAGACGGACAAATAAAAAAAGATTAAGAGACCAGTAGCGCC
V I K N R K F H F P F Y Y L L A N L A A
421 CAGTGATCAAAAACAGAAAATTTCAATTTCCCTTTTACTACCTGTTGGCTAATTTAGCTG 480
-----+-----+-----+-----+-----+-----+-----+
GTCAGTAGTTTTTGTCTTTTAAAGTAAAGGGGAAATGATGGACAACCGATTAAATCGAC
A D F F A G I A Y V F L M F N T G P V S
481 CTGCCGATTTCTTCGCTGGAATTGCCTATGTATTCCTGATGTTTAACACAGGCCAGTTT 540
-----+-----+-----+-----+-----+-----+-----+
GACGGCTAAAGAAGCGACCTTAACGGATACATAAGGACTACAAATTGTGTCCGGGTCAAA
K T L T V N R W F L R Q G L L D S S L T
541 CAAAACTTTGACTGTCAACCGCTGGTTTCTCCGTCAGGGGCTTCTGGACAGTAGCTTGA 600
-----+-----+-----+-----+-----+-----+-----+
GTTTTTGAACTGACAGTTGGCGACCAAAGAGGCAGTCCCCGAAGACCTGTCATCGAACT

Figure 4A (cont.)



601 A S L T N L L V I A V E R H M S I M R M
CTGCTTCCCTCACCAACTTGCTGGTTATCGCCGTGGAGAGGCACATGTCAATCATGAGGA
-----+-----+-----+-----+-----+-----+-----+ 660
GACGAAGGGAGTGTTGAACGACCAATAGCGGCACCTCTCCGTGTACAGTTAGTACTCCT

661 R V H S N L T K K R V T L L I L L V W A
TGCGGGTCCATAGCAACCTGACCAAAAAGAGGGTGACACTGCTCATTTTGCTTGTCTGGG
-----+-----+-----+-----+-----+-----+-----+ 720
ACGCCAGGTATCGTTGGACTGGTTTTTCTCCACTGTGACGAGTAAACGAACAGACCC

721 I A I F M G A V P T L G W N C L C N I S
CCATCGCCATTTTATGGGGGCGGTCCCCACACTGGGCTGGAATTGCCTCTGCAACATCT
-----+-----+-----+-----+-----+-----+-----+ 780
GGTAGCGGTAAAAATACCCCCGCCAGGGGTGTGACCCGACCTTAACGGAGACGTTGTAGA

781 A C S S L A P I Y S R S Y L V F W T V S
CTGCCTGCTCTTCCCTGGCCCCCATTTACAGCAGGAGTTACCTTGTTTTCTGGACAGTGT
-----+-----+-----+-----+-----+-----+-----+ 840
GACGGACGAGAAGGGACCGGGGTAAATGTCGTCCTCAATGGAACAAAAGACCTGTCACA

841 N L M A F L I M V V V Y L R I Y V Y V K
CCAACCTCATGGCCTTCTCATCATGTTGTGGTGTACCTGCGGATCTACGTGTACGTCA
-----+-----+-----+-----+-----+-----+-----+ 900
GGTTGGAGTACCGGAAGGAGTAGTACCAACACCACATGGACGCCTAGATGCACATGCAGT

901 R K T N V L S P H T S G S I S R R R T P
AGAGGAAAACCAACGTCTTGTCTCCGCATACAAGTGGGTCCATCAGCCGCCGGAGGACAC
-----+-----+-----+-----+-----+-----+-----+ 960
TCTCCTTTTGGTTGCAGAACAGAGGCGTATGTTCACCCAGGTAGTCGGCGGCCTCCTGTG

961 M K L M K T V M T V L G A F V V C W T P
CCATGAAGCTAATGAAGACGGTGATGACTGTCTTAGGGGCGTTTGTGGTATGCTGGACCC
-----+-----+-----+-----+-----+-----+-----+ 1020
GGTACTTCGATTACTTCTGCCACTACTGACAGAATCCCCGAAACACCATACGACCTGGG

1021 G L V V L P L D G L N C R Q C G V Q H V
CGGGCCTGGTGGTTCTGCCCCCTCGACGGCCTGAACTGCAGGCAGTGTGGCGTGCAGCATG
-----+-----+-----+-----+-----+-----+-----+ 1080
GCCCCGACCACCAAGACGGGGAGCTGCCGGACTTGACGTCCGTACACCCGCACGTCGTAC

1081 K R W F L L L A L L N S V V N P I I Y S
TGAAAAGGTGGTTCTGCTGCTGGCGCTGCTCAACTCCGTCTGTAACCCCATCATCTACT
-----+-----+-----+-----+-----+-----+-----+ 1140
ACTTTTCCACCAAGGACGACGACCGCGACGAGTTGAGGCAGCACTTGGGGTAGTAGATGA

1141 Y K D E D M Y G T M K K M I C C F S Q E
CCTACAAGGACGAGGACATGTATGGCACCATGAAGAAGATGATCTGCTGCTTCTCTCAGG
-----+-----+-----+-----+-----+-----+-----+ 1200
GGATGTTCTGCTCCTGTACATACCGTGGTACTTCTTCTACTAGACGACGAAGAGAGTCC

1201 N P E R R P S R I P S T V L S R S D T G
AGAACCCAGAGAGGCGTCCCTCTCGCATCCCCCTCCACAGTCTCAGCAGGAGTGACACAG
-----+-----+-----+-----+-----+-----+-----+ 1260
TCTTGGGTCTCTCCGCAGGGAGAGCGTAGGGGAGGTGTGAGGAGTCGTCTCTCACTGTGTC

1261 S Q Y I E D S I S Q G A V C N K S T S *
GCAGCCAGTACATAGAGGATAGTATTAGCCAAGGTGCAGTCTGCAATAAAAGCACTTCCT
-----+-----+-----+-----+-----+-----+-----+ 1320
CGTCGGTCATGTATCTCCTATCATAATCGGTTCCACGTGACGCGTTATTTTCGTGAAGGA



Figure 4A (cont.)

	AAACTCTGGATGCCCTCTYGGCCACCAGGCCTCCTCTGGGAAAAGAGCTGTTAAGAATG	
1321	- - - + - - - + - - - + - - - + - - - + - - - + - - - +	1380
	TTTGAGACCTACGGAGARCCGGTGGGTCCGGAGGAGACCCCTTTCTCGACAATTCTTAC	
	ATTACCTGTCTCTAACAAAGCCCATGTACAGTGTTATTTGAGGTCTCCATTAATCACTGC	
1381	- - - + - - - + - - - + - - - + - - - + - - - +	1440
	TAATGGACAGAGATTGTTTTCGGGTACATGTCACAATAAACTCCAGAGGTAATTAGTGACG	
	TAGATTTCTTTAAAAAATTTTTTTTCATAGTTTAAAAGCATGGGCAGTAAAGAGAGGACC	
1441	- - - + - - - + - - - + - - - + - - - + - - - +	1500
	ATCTAAAGAAATTTTTTAAAAAAAGTATCAAATTTTCGTACCCGTCATTTCTCTCCTGG	
	TGCTGCATTTAGAGAAAGCACAG	
1501	- - - + - - - + - - - + - - - + - - - + - - - +	1523
	ACGACGTAAATCTCTTTCGTGTC	

Figure 4B: Predicted amino acid sequence of hEDG5 encoded by clone pC3-hEDG5#3.4

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1  MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFP CLFIFFSNSL
51  VIAAVIKNRK FHFPFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN
101 RWFLRQGLLD SSLTASLTNL LVIAVERHMS IMRMRVHSNL TKKRVTLILL
151 LVWAIAIFMG AVPTLGWNCL CNISACSSLA PIYSRSYLVF WTVSNLMAFL
201 IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT VMTVLGAFVV
251 CWTPLGVVLL LDGLNCRQCG VQHVKRWFL LALLNSVVNP IIYSYKDEDM
301 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK
351 STS

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Figure 4C: Predicted amino acid sequence of hEDG5 encoded by clone pC3-hEDG5#28.

1	MNECHYDKHM	DDFYNRGNTD	TVDDWTGTLK	VIVLCVGTFF	CLFIFFSNSL
51	VIAAVIKNRK	FHFPPFYLLA	NLAAADFFAG	IAYVFLMFT	GPVSKTLTVN
101	RWFLRQGLLD	SSLTASLTNL	LVIAYERHMS	IMMRVHSNL	TKKRVTLILL
151	LVWAIAIFMG	AVPTLGWNCL	CNISACSSLA	PIYSRSYLVF	WTVSNLMAFL
201	IMVVYLRIY	VYVKRKTNVL	SPHTSGSISR	RRTPMKLMKT	VMTVLGAFVV
251	CWTPGLVLL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVNP	IIYSYKDEDM
301	YGTMKKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK
351	STS				

pC3-hedg55 has been
replaced.



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      caccttcctaacctgagcgccctagcctgggaaacaaacaattaaaatgtgcgctaaatg
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
      gtggaaggattggactcgccgatcgacccttggttgttaattttacacgcgatttac
      ctgtggttaggaggtcaggggctatgtcctggaccaaaggacatttgcactgagacctgac
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
      gacaccatcctccagtcctccgatacaggacctggtttcctgtaaactgactctggactg
      acttcaggtcttcaactccttggatgggagttagccagaacgggcttagaaacagcaatt
121  -----+-----+-----+-----+-----+-----+-----+-----+ 180
      tgaagtccagaagttgaggggaactaccctcaatcggctctgcccgaatctttgtcgtaaa
      gatggcttagtgactgattttacaaatgatatttgtttcttctttaatttctttcttagg
181  -----+-----+-----+-----+-----+-----+-----+-----+ 240
      ctaccgaatcactgactaaaaatgtttactataaacaagaagaatttaagaaagatcc
      M N E C H Y D K H M D F F Y
      atgttcacttCTTCTCCACAATGAATGAGTGTCACTATGACAAGCACATGGACTTTTTTT
241  -----+-----+-----+-----+-----+-----+-----+-----+ 300
      tacaagtgaagaagAGGTGTTACTTACTCACAGTGATACTGTTTCGTGTACCTGAAAAAAA
      N R S N T D T V D D W T G T K L V I V L
      ATAATAGGAGCAACACTGATACTGTGATGACTGGACAGGAACAAAGCTTGTGATTGTTT
301  -----+-----+-----+-----+-----+-----+-----+-----+ 360
      TATTATCCTCGTTGTGACTATGACAGCTACTGACCTGTCCTTGTTCGAACACTAACAAA
      C V G T F F C L F I F F S N S L V I A A
      TGTGTGTTGGGACGTTTTTCTGCCTGTTTATTTTTTTTTTCTAATTCTCTGGTCATCGCGG
361  -----+-----+-----+-----+-----+-----+-----+-----+ 420
      ACACACAACCCTGCAAAAAGACGGACAAATAAAAAAAGATTAAGAGACCAGTAGCGCC
      V I K N R K F H F P F Y Y L L A N L A A
      CAGTGATCAAAAACAGAAAATTTTCAATTTCCCTTTTACTACCTGTTGGCTAATTTAGCTG
421  -----+-----+-----+-----+-----+-----+-----+-----+ 480
      GTCAGTAGTTTTTGTCTTTTAAAGTAAAGGGGAAAATGATGGACAACCGATTAAATCGAC
      A D F F A G I A Y V F L M F N T G P V S
      CTGCCGATTTCTTCGCTGGAATTGCCTATGTATTCTGTATGTTTAACACAGGCCAGTTT
481  -----+-----+-----+-----+-----+-----+-----+-----+ 540
      GACGGCTAAAGAAGCGACCTTAACGGATACATAAGGACTACAAATTGTGTCGGGTCAAA
      K T L T V N R W F L R Q G L L D S S L T
      CAAAACTTTGACTGTCAACCGCTGGTTTCTCCGTCAGGGGCTTCTGGACAGTAGCTTGA
541  -----+-----+-----+-----+-----+-----+-----+-----+ 600
      GTTTTTGAACTGACAGTTGGCGACCAAGAGGCAGTCCCCGAAGACCTGTCATCGAACT

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